

In re application of : REGENTS OF THE UNIVERSITY OF MINNESOTA et al.
Application Serial No. : PCT/US97/22125
Filed : 05 December 1997
Agent Ref. : 600.347WOI1
Title : MUTANTS OF STREPTOCOCCAL TOXIN C AND
METHODS OF USE

RESPONSE TO INVITATION TO
FURNISH NUCLEOTIDE AND/OR AMINO ACID SEQUENCE LISTING

International Searching Authority
European Patent Office
*Storage and Retrieval of Amino
acid and Nucleotide Data*
Patentlaan 2
P.O. 5818
NL-2280 HV Rijswijk
NETHERLANDS

Dear Sir:

In connection with the INVITATION TO FURNISH NUCLEOTIDE AND/OR AMINO ACID SEQUENCE LISTING mailed on 16 February 1998, Applicants hereby furnish the SEQUENCE LISTING in computer readable form, complying with WIPO Standard ST.23, as recited at pages 40a-40c of the above-captioned application.

It is respectfully submitted that the contents of the paper version of the SEQUENCE LISTING and the computer readable version of the SEQUENCE LISTING, both of which are submitted herewith, are the same.

Respectfully submitted,

MERCHANT, GOULD, SMITH, EDELL,
WELTER & SCHMIDT, P.A.

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Minneapolis, Minnesota 55402
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Dated: March 26, 1998

By Steven C. Bruess
Steven C. Bruess
Reg. No. 34,130

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Regents of the University of Minnesota
- (ii) TITLE OF THE INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN C
AND METHODS OF USE
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
 - (B) STREET: 3100 Norwest Center, 90 South 7th Street
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US97/22125
 - (B) FILING DATE: 05-DEC-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/033,251
 - (B) FILING DATE: 06-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Skoog, Mark T
 - (B) REGISTRATION NUMBER: 40,178
 - (C) REFERENCE/DOCKET NUMBER: 600.347WO11
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612-332-5300
 - (B) TELEFAX: 612-332-9081
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 154...858
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAACCTTGAC TATTTAAATG GAACTGCCAC TCCTAAAAC TAAAATATAA ATACATTTAT	60
AAAATTTCTA AATAAACAGA AATCTGATTT TTAAGTACTT ACTGCTATTT CATGTATTCT	120
CGTACGAGTA ATACATTTAA TTAAGGAGAA AAA ATG AAA AAG ATT AAC ATC ATC	174
Met Lys Lys Ile Asn Ile Ile	
1 5	
AAA ATA GTT TTC ATA ATT ACA GTC ATA CTG ATT TCT ACT TAT TTC ACC	222
Lys Ile Val Phe Ile Ile Thr Val Ile Leu Ile Ser Thr Tyr Phe Thr	
10 15 20	
TAT CAT CAA AGT GAC TCT AAG AAA GAC ATT TCG AAT GTT AAA AGT GAT	270
Tyr His Gln Ser Asp Ser Lys Lys Asp Ile Ser Asn Val Lys Ser Asp	
25 30 35	
TTA CTT TAT GCA TAC ACT ATA ACT CCT TAT GAT TAT AAA GAT TGC AGG	318
Leu Leu Tyr Ala Tyr Thr Ile Thr Pro Tyr Asp Tyr Lys Asp Cys Arg	
40 45 50 55	
GTA AAT TTT TCA ACG ACA CAC ACA TTA AAC ATT GAT ACT CAA AAA TAT	366
Val Asn Phe Ser Thr Thr His Thr Leu Asn Ile Asp Thr Gln Lys Tyr	
60 65 70	
AGA GGG AAA GAC TAT TAT ATT AGT TCC GAA ATG TCT TAT GAG GCC TCT	414
Arg Gly Lys Asp Tyr Tyr Ile Ser Ser Glu Met Ser Tyr Glu Ala Ser	
75 80 85	
CAA AAA TTT AAA CGA GAT GAT CAT GTA GAT GTT TTT GGA TTA TTT TAT	462
Gln Lys Phe Lys Arg Asp Asp His Val Asp Val Phe Gly Leu Phe Tyr	
90 95 100	
ATT CTT AAT TCT CAC ACC GGT GAG TAC ATC TAT GGA GGA ATT ACG CCT	510
Ile Leu Asn Ser His Thr Gly Glu Tyr Ile Tyr Gly Gly Ile Thr Pro	
105 110 115	
GCT CAA AAT AAT AAA GTA AAT CAT AAA TTA TTG GGA AAT CTA TTT ATT	558
Ala Gln Asn Asn Lys Val Asn His Lys Leu Leu Gly Asn Leu Phe Ile	
120 125 130 135	
TCG GGA GAA TCT CAA CAG AAC TTA AAT AAC AAG ATT ATT CTA GAA AAG	606
Ser Gly Glu Ser Gln Gln Asn Leu Asn Asn Lys Ile Ile Leu Glu Lys	
140 145 150	
GAT ATC GTA ACT TTC CAG GAA ATT GAC TTT AAA ATC AGA AAA TAC CTT	654
Asp Ile Val Thr Phe Gln Glu Ile Asp Phe Lys Ile Arg Lys Tyr Leu	
155 160 165	

ATG GAT AAT TAT AAA ATT TAT GAC GCT ACT TCT CCT TAT GTA AGC GGC Met Asp Asn Tyr Lys Ile Tyr Asp Ala Thr Ser Pro Tyr Val Ser Gly 170 175 180	702
AGA ATC GAA ATT GGC ACA AAA GAT GGG AAA CAT GAG CAA ATA GAC TTA Arg Ile Glu Ile Gly Thr Lys Asp Gly Lys His Glu Gln Ile Asp Leu 185 190 195	750
TTT GAC TCA CCA AAT GAA GGG ACT AGA TCA GAT ATT TTT GCA AAA TAT Phe Asp Ser Pro Asn Glu Gly Thr Arg Ser Asp Ile Phe Ala Lys Tyr 200 205 210 215	798
AAA GAT AAT AGA ATT ATC AAT ATG AAG AAC TTT AGT CAT TTC GAT ATT Lys Asp Asn Arg Ile Ile Asn Met Lys Asn Phe Ser His Phe Asp Ile 220 225 230	846
TAT CTT GAA AAA TAATTCATCA TACACAAAAA ACCGCCCCAGA ATAATCTGAG CGGTT Tyr Leu Glu Lys 235	903
TTGTCTTATC TCGGAGCTTT ACCTCCTAAT TTA	936

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Lys Ile Asn Ile Ile Lys Ile Val Phe Ile Ile Thr Val Ile 1 5 10 15
Leu Ile Ser Thr Tyr Phe Thr Tyr His Gln Ser Asp Ser Lys Lys Asp 20 25 30
Ile Ser Asn Val Lys Ser Asp Leu Tyr Ala Tyr Thr Ile Thr Pro 35 40 45
Tyr Asp Tyr Lys Asp Cys Arg Val Asn Phe Ser Thr Thr His Thr Leu 50 55 60
Asn Ile Asp Thr Gln Lys Tyr Arg Gly Lys Asp Tyr Tyr Ile Ser Ser 65 70 75 80
Glu Met Ser Tyr Glu Ala Ser Gln Lys Phe Lys Arg Asp Asp His Val 85 90 95
Asp Val Phe Gly Leu Phe Tyr Ile Leu Asn Ser His Thr Gly Glu Tyr 100 105 110
Ile Tyr Gly Gly Ile Thr Pro Ala Gln Asn Asn Lys Val Asn His Lys 115 120 125
Leu Leu Gly Asn Leu Phe Ile Ser Gly Glu Ser Gln Gln Asn Leu Asn 130 135 140
Asn Lys Ile Ile Leu Glu Lys Asp Ile Val Thr Phe Gln Glu Ile Asp 145 150 155 160
Phe Lys Ile Arg Lys Tyr Leu Met Asp Asn Tyr Lys Ile Tyr Asp Ala 165 170 175
Thr Ser Pro Tyr Val Ser Gly Arg Ile Glu Ile Gly Thr Lys Asp Gly 180 185 190
Lys His Glu Gln Ile Asp Leu Phe Asp Ser Pro Asn Glu Gly Thr Arg 195 200 205
Ser Asp Ile Phe Ala Lys Tyr Lys Asp Asn Arg Ile Ile Asn Met Lys 210 215 220
Asn Phe Ser His Phe Asp Ile Tyr Leu Glu Lys 225 230 235